

0701012W01.ST25.txt
SEQUENCE LISTING

<110> Kureha Chemical Industry Company, Limited
KAMATA, Toru
MITSUSHITA, Junji

<120> Antibodies to Nox1 polypeptide, method for the detection of cancer using Nox1 gene and method for screening substances suppressing cancer growth

<130> 0701012W01

<160> 27

<170> PatentIn version 3.1

<210> 1

<211> 1734

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (71)..(1618)

<223> Human Nox1 polypeptide of SEQ NO:2

<400> 1
ggacctctcc agaatccgga ttgctgaatc ttccctgttg cctagaaggg ctccaaacca 60
cctcttgaca atg gga aac tgg gtg gtt aac cac tgg ttt tca gtt ttg 109
Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu
1 5 10
ttt ctg gtt gtt tgg tta ggg ctg aat gtt ttc ctg ttt gtg gat gcc 157
Phe Leu Val Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala
15 20 25
ttc ctg aaa tat gag aag gcc gac aaa tac tac tac aca aga aaa atc 205
Phe Leu Lys Tyr Glu Lys Ala Asp Lys Tyr Tyr Thr Arg Lys Ile
30 35 40 45
ctt ggg tca aca ttg gcc tgt gcc cga gcg tct gct ctc tgc ttg aat 253
Leu Gly Ser Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn
50 55 60

0701012W01.ST25.txt

ttt	aac	agc	acg	ctg	atc	ctg	ctt	cct	gtg	tgt	cgc	aat	ctg	ctg	tcc	301
Phe	Asn	Ser	Thr	Leu	Ile	Leu	Leu	Pro	Val	Cys	Arg	Asn	Leu	Leu	Ser	
			65					70					75			
ttc	ctg	agg	ggc	acc	tgc	tca	ttt	tgc	agc	cgc	aca	ctg	aga	aag	caa	349
Phe	Leu	Arg	Gly	Thr	Cys	Ser	Phe	Cys	Ser	Arg	Thr	Leu	Arg	Lys	Gln	
		80					85					90				
ttg	gat	cac	aac	ctc	acc	ttc	cac	aag	ctg	gtg	gcc	tat	atg	atc	tgc	397
Leu	Asp	His	Asn	Leu	Thr	Phe	His	Lys	Leu	Val	Ala	Tyr	Met	Ile	Cys	
	95					100					105					
cta	cat	aca	gct	att	cac	atc	att	gca	cac	ctg	ttt	aac	ttt	gac	tgc	445
Leu	His	Thr	Ala	Ile	His	Ile	Ile	Ala	His	Leu	Phe	Asn	Phe	Asp	Cys	
					115					120					125	
tat	agc	aga	agc	cga	cag	gcc	aca	gat	ggc	tcc	ctt	gcc	tcc	att	ctc	493
Tyr	Ser	Arg	Ser	Arg	Gln	Ala	Thr	Asp	Gly	Ser	Leu	Ala	Ser	Ile	Leu	
				130					135					140		
tcc	agc	cta	tct	cat	gat	gag	aaa	aag	ggg	ggg	tct	tgg	cta	aat	ccc	541
Ser	Ser	Leu	Ser	His	Asp	Glu	Lys	Lys	Gly	Gly	Ser	Trp	Leu	Asn	Pro	
			145					150					155			
atc	cag	tcc	cga	aac	acg	aca	gtg	gag	tat	gtg	aca	ttc	acc	agc	att	589
Ile	Gln	Ser	Arg	Asn	Thr	Thr	Val	Glu	Tyr	Val	Thr	Phe	Thr	Ser	Ile	
			160				165					170				
gct	ggg	ctc	act	gga	gtg	atc	atg	aca	ata	gcc	ttg	att	ctc	atg	gta	637
Ala	Gly	Leu	Thr	Gly	Val	Ile	Met	Thr	Ile	Ala	Leu	Ile	Leu	Met	Val	
	175					180					185					
act	tca	gct	act	gag	ttc	atc	cgg	agg	agt	tat	ttt	gaa	gtc	ttc	tgg	685
Thr	Ser	Ala	Thr	Glu	Phe	Ile	Arg	Arg	Ser	Tyr	Phe	Glu	Val	Phe	Trp	
					195					200					205	
tat	act	cac	cac	ctt	ttt	atc	ttc	tat	atc	ctt	ggc	tta	ggg	att	cac	733
Tyr	Thr	His	His	Leu	Phe	Ile	Phe	Tyr	Ile	Leu	Gly	Leu	Gly	Ile	His	
				210					215					220		
ggc	att	ggg	gga	att	gtc	cgg	ggg	caa	aca	gag	gag	agc	atg	aat	gag	781
Gly	Ile	Gly	Gly	Ile	Val	Arg	Gly	Gln	Thr	Glu	Glu	Ser	Met	Asn	Glu	
			225					230					235			
agt	cat	cct	cgc	aag	tgt	gca	gag	tct	ttt	gag	atg	tgg	gat	gat	cgt	829
Ser	His	Pro	Arg	Lys	Cys	Ala	Glu	Ser	Phe	Glu	Met	Trp	Asp	Asp	Arg	
		240					245					250				
gac	tcc	cac	tgt	agg	cgc	cct	aag	ttt	gaa	ggg	cat	ccc	cct	gag	tct	877
Asp	Ser	His	Cys	Arg	Arg	Pro	Lys	Phe	Glu	Gly	His	Pro	Pro	Glu	Ser	
						260					265					
tgg	aag	tgg	atc	ctt	gca	ccg	gtc	att	ctt	tat	atc	tgt	gaa	agg	atc	925
Trp	Lys	Trp	Ile	Leu	Ala	Pro	Val	Ile	Leu	Tyr	Ile	Cys	Glu	Arg	Ile	
					275					280					285	
ctc	cgg	ttt	tac	cgc	tcc	cag	cag	aag	gtt	gtg	att	acc	aag	gtt	gtt	973
Leu	Arg	Phe	Tyr	Arg	Ser	Gln	Gln	Lys	Val	Val	Ile	Thr	Lys	Val	Val	
				290					295					300		
atg	cac	cca	tcc	aaa	gtt	ttg	gaa	ttg	cag	atg	aac	aag	cgt	ggc	ttc	1021
Met	His	Pro	Ser	Lys	Val	Leu	Glu	Leu	Gln	Met	Asn	Lys	Arg	Gly	Phe	
			305					310					315			
agc	atg	gaa	gtg	ggg	cag	tat	atc	ttt	gtt	aat	tgc	ccc	tca	atc	tct	1069
Ser	Met	Glu	Val	Gly	Gln	Tyr	Ile	Phe	Val	Asn	Cys	Pro	Ser	Ile	Ser	

0701012W01.ST25.txt

320	325	330	
ctc ctg gaa tgg cat cct ttt act ttg acc tct gct cca gag gaa gat			1117
Leu Leu Glu Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp			
335	340	345	
ttc ttc tcc att cat atc cga gca gca ggg gac ttg aca gaa aat ctc			1165
Phe Phe Ser Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu			
350	355	360	
ata agg gct ttc gaa caa caa tat tca cca att ccc agg att gaa gtg			1213
Ile Arg Ala Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val			
370	375	380	
gat ggt ccc ttt ggc aca gcc agt gag gat gtt ttc cag tat gaa gtg			1261
Asp Gly Pro Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val			
385	390	395	
gct gtg ctg gtt gga gca gga att ggg gtc acc ccc ttt gct tct atc			1309
Ala Val Leu Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile			
400	405	410	
ttg aaa tcc atc tgg tac aaa ttc cag tgt gca gac cac aac ctc aaa			1357
Leu Lys Ser Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys			
415	420	425	
aca aaa aag gtt ggt cat gca gca tta aac ttt gac aag gcc act gac			1405
Thr Lys Lys Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp			
430	435	440	
atc gtg aca ggt ctg aaa cag aaa acc tcc ttt ggg aga cca atg ttg			1453
Ile Val Thr Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp			
450	455	460	
gac aat gag ttt tct aca ata gct acc tcc cac ccc aag tct gta gtg			1501
Asp Asn Glu Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val			
465	470	475	
gga gtt ttc tta tgt ggc cct cgg act ttg gca aag agc ctg cgc aaa			1549
Gly Val Phe Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys			
480	485	490	
tgc tgt cac cga tat tcc agt ctg gat cct aga aag gtt caa ttc tac			1597
Cys Cys His Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr			
495	500	505	
ttc aac aaa gaa aat ttt tga gttataggaa taaggacggt aatctgcatt			1648
Phe Asn Lys Glu Asn Phe			
510	515		
ttgtctcttt gtatcttcag taattttactt ggtctctgca ggtttgagca gtcacttttag			1708
gataagaatg tgcctctcaa gccttg			1734

<210> 2

<211> 515

<212> PRT

<213> Homo sapiens

<400> 2

0701012wo1.ST25.txt

Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu Phe Leu Val
1 5 10 15

Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys
20 25 30

Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
35 40 45

Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
50 55 60

Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
65 70 75 80

Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His
85 90 95

Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr
100 105 110

Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg
115 120 125

Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu
130 135 140

Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile Gln Ser
145 150 155 160

Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Ile Ala Gly Leu
165 170 175

Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala
180 185 190

Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His
195 200 205

His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly
210 215 220

Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro
225 230 235 240

Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His
245 250 255

Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp
260 265 270

Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile Leu Arg Phe
 275 280 285

Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro
 290 295 300

Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe Ser Met Glu
 305 310 315 320

Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Leu Leu Glu
 325 330 335

Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser
 340 345 350

Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Ala
 355 360 365

Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val Asp Gly Pro
 370 375 380

Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu
 385 390 395 400

Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser
 405 410 415

Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys Thr Lys Lys
 420 425 430

Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr
 435 440 445

Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu
 450 455 460

Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val Phe
 465 470 475 480

Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys His
 485 490 495

Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe Asn Lys
 500 505 510

Glu Asn Phe
 515

<210> 3

<211> 2577

<212> DNA

<213> Rattus norvegicus

<220>

<221> CDS

<222> (128)..(1819)

<223> Rat Nox1 polypeptide of SEQ NO:4

<400> 3

```

ttctgagtag gtgtgcattt gagtgtcata aagacatata tcttgagcta gacagaagtt      60
cctatcctga aggatcccat cagagaaacc agattgctcc taagaggctc cagacctcca      120
tttgaca atg gga aac tgg ctg gtt aac cac tgg ctc tca gtt ttg ttt      169
          Met Gly Asn Trp 5 Val Asn His Trp 10 Ser Val Leu Phe
ctg gtt tct tgg ttg ggg ctg aac att ttt ctg ttt gtg tac gtc ttc      217
Leu Val Ser Trp Leu 20 Gly Leu Asn Ile Phe 25 Leu Phe Val Tyr Val Phe 30
ctg aat tat gag aag tct gac aag tac tat tac acg aga gaa att ctc      265
Leu Asn Tyr Glu 35 Lys Ser Asp Lys Tyr 40 Tyr Thr Arg Glu 45 Ile Leu
gga act gcc ttg gcc ttg gcc aga gca tct gct ttg tgc ctg aat ttt      313
Gly Thr Ala Leu 50 Ala Leu Ala Arg Ala 55 Ser Ala Leu Cys Leu 60 Asn Phe
aac agc atg gtg atc ctg att cct gtg tgt cga aat ctg ctc tcc ttc      361
Asn Ser Met 65 Val Ile Leu Ile Pro 70 Val Cys Arg Asn Leu 75 Leu Ser Phe
ctg agg ggc acc tgc tca ttt tgc aac cac acg ctg aga aag cca ttg      409
Leu Arg Gly Thr Cys Ser Phe 85 Cys Asn His Thr 90 Leu Arg Lys Pro Leu
gat cac aac ctc acc ttc cat aag ctg gtg gca tat atg atc tgc ata      457
Asp His Asn Leu Thr 100 Phe His Lys Leu Val 105 Ala Tyr Met Ile Cys 110 Ile
ttc aca gct att cat atc att gca cat cta ttt aac ttt gaa cgc tac      505
Phe Thr Ala Ile 115 His Ile Ile Ala His Leu 120 Phe Asn Phe Glu 125 Arg Tyr
agt aga agc caa cag gcc atg gat gga tct ctt gcc tct gtt ctc tcc      553
Ser Arg Ser Gln Gln Ala Met Asp Gly 135 Ser Leu Ala Ser Val 140 Leu Ser
agc cta ttc cat ccc gag aaa gaa gat tct tgg cta aat ccc atc cag      601
Ser Leu Phe His Pro Glu Lys 150 Glu Asp Ser Trp Leu 155 Asn Pro Ile Gln
tct cca aac gtg aca gtg atg tat gca gca ttt acc agt att gct ggc      649
Ser Pro Asn Val Thr Val 165 Met Tyr Ala Ala Phe Thr 170 Ser Ile Ala Gly

```

0701012w01.ST25.txt

ctt Leu 175	act Thr	gga Gly	gtg Val	gtc Val	gcc Ala 180	act Thr	gtg Val	gct Ala	tgg Leu	gtt Val 185	ctc Leu	atg Met	gta Val	act Thr	tca Ser 190	697
gct Ala	atg Met	gag Glu	ttt Phe	atc Ile 195	cgc Arg	agg Arg	aat Asn	tat Tyr	ttt Phe 200	gag Glu	ctc Leu	ttc Phe	tgg Trp	tat Tyr 205	aca Thr	745
cat His	cac His	ctt Leu	ttc Phe 210	atc Ile	atc Ile	tat Tyr	atc Ile 215	atc Ile	tgc Cys	tta Leu	ggg Gly	atc Ile 220	cat His	ggc Gly	ctg Leu	793
ggg Gly	ggg Gly	att Ile 225	gtc Val	cgg Arg	ggg Gly	caa Gln 230	aca Thr	gaa Glu	gag Glu	agc Ser	atg Met	agt Ser 235	gaa Glu	agt Ser	cat His	841
ccc Pro	cgc Arg 240	aac Asn	tgt Cys	tca Ser	tac Tyr	tct Ser 245	ttc Phe	cac His	gag Glu	tgg Trp	gat Asp 250	aag Lys	tat Tyr	gaa Glu	agg Arg	889
agt Ser 255	tgc Cys	agg Arg	agt Ser	cct Pro	cat His 260	ttt Phe	gtg Val	ggg Gly	caa Gln 265	ccc Pro	cct Pro	gag Glu	tct Ser	tgg Trp	aag Lys 270	937
tgg Trp	atc Ile	ctc Leu	gcg Ala 275	ccg Pro	att Ile	gct Ala	ttt Phe	tat Tyr	atc Ile 280	ttt Phe	gaa Glu	agg Arg	atc Ile	ctt Leu 285	cgc Arg	985
ttt Phe	tat Tyr	cgc Arg	tcc Ser 290	cgg Arg	cag Gln	aag Lys	gtc Val	gtg Val 295	att Ile	acc Thr	aag Lys	gtt Val	gtc Val 300	atg Met	cac His	1033
cca Pro	tgt Cys	aaa Lys 305	gtt Val	ttg Leu	gaa Glu	ttg Leu	cag Gln 310	atg Met	agg Arg	aag Lys	cgg Arg	ggc Gly 315	ttt Phe	act Thr	atg Met	1081
gga Gly	ata Ile 320	gga Gly	cag Gln	tat Tyr	ata Ile	ttc Phe 325	gta Val	aat Asn	tgc Cys	ccc Pro	tcg Ser 330	att Ile	tcc Ser	ttc Phe	ctg Leu	1129
gaa Glu 335	tgg Trp	cat His	ccc Pro	ttt Phe	act Thr 340	ctg Leu	acc Thr	tct Ser	gct Ala	cca Pro 345	gag Glu	gaa Glu	gaa Glu	ttt Phe	ttc Phe 350	1177
tcc Ser	att Ile	cat His	att Ile	cga Arg 355	gca Ala	gca Ala	ggg Gly	gac Asp	tgg Trp 360	aca Thr	gaa Glu	aat Asn	ctc Leu	ata Ile 365	agg Arg	1225
aca Thr	ttt Phe	gaa Glu 370	caa Gln	cag Gln	cac His	tca Ser	cca Pro	atg Met 375	ccc Pro	agg Arg	atc Ile	gag Glu	gtg Val 380	gat Asp	ggg Gly	1273
ccc Pro	ttt Phe	ggc Gly 385	aca Thr	gtc Val	agt Ser	gag Glu	gat Asp 390	gtc Val	ttc Phe	cag Gln	tac Tyr	gaa Glu 395	gtg Val	gct Ala	gta Val	1321
ctg Leu 400	gtt Val	ggg Gly	gca Ala	ggg Gly	att Ile	ggc Gly 405	gtc Val	act Thr	ccc Pro	ttt Phe	gct Ala 410	tcc Ser	ttc Phe	ttg Leu	aaa Lys	1369
tct Ser 415	atc Ile	tgg Trp	tac Tyr	aaa Lys	ttc Phe 420	cag Gln	cgt Arg	gca Ala	cac His	aac Asn 425	aag Lys	ctg Leu	aaa Lys	aca Thr	caa Gln 430	1417
aag Lys	atc Ile	tat Tyr	ttc Phe	tac Tyr 435	tgg Trp	att Ile	tgt Cys	aga Arg	gag Glu 440	acg Thr	ggg Gly	gcc Ala	ttt Phe	gcc Ala 445	tgg Trp	1465

0701012W01.ST25.txt

ttc aac aac tta ttg aat tcc ctg gaa caa gag atg gac gaa tta ggc Phe Asn Asn Leu Leu Asn Ser Leu Glu Gln Glu Met Asp Glu Leu Gly 450 455 460	1513
aaa ccg gat ttc cta aac tac cga ctc ttc ctc act ggc tgg gat agc Lys Pro Asp Phe Leu Asn Tyr Arg Leu Phe Leu Thr Gly Trp Asp Ser 465 470 475	1561
aac att gct ggt cat gca gca tta aac ttt gac aga gcc act gac gtc Asn Ile Ala Gly His Ala Ala Leu Asn Phe Asp Arg Ala Thr Asp Val 480 485 490	1609
ctg aca ggt ctg aaa cag aaa acc tcc ttt ggg aga cca atg tgg gac Leu Thr Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp 495 500 505 510	1657
aat gag ttt tct aga ata gct act gcc cac ccc aag tct gtg gtg ggg Asn Glu Phe Ser Arg Ile Ala Thr Ala His Pro Lys Ser Val Val Gly 515 520 525	1705
gtt ttc tta tgc ggc cct ccg act ttg gca aaa agc ctg cgc aaa tgc Val Phe Leu Cys Gly Pro Pro Thr Leu Ala Lys Ser Leu Arg Lys Cys 530 535 540	1753
tgt cgg cgg tac tca agt ctg gat cct agg aag gtt caa ttc tac ttc Cys Arg Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe 545 550 555	1801
aac aaa gaa acg ttc tga attggaggaa gccgcacagt agtacttctc Asn Lys Glu Thr Phe 560	1849
catcttcctt ttcactaacg tgtgggtcag ctactagata gtccgttgtc gcacaaggac	1909
ttcactccca tcttaaagtt gactcaactc catcattctt gggctttggc aacatgagag	1969
ctgcataact cacaattgca aaacacatga attattattg gggggattgt aaatccttct	2029
gggaaacctg cctttagctg aatcttgctg gttgacactt gcacaattta acctcagggtg	2089
tcttggttga tacctgataa tcttccctcc cacctgtccc tcacagaaga tttctaagta	2149
gggtgatttt aaaatattta ttgaatccac gacaaaacaa taatcataaa taataaacat	2209
aaaattacca agattccac tcccatatca taccactaa gaacatcggt atacatgagc	2269
ttatcatcca gtgtgaccaa caatttatac tttactgtgc caaaataatc ttcattcttg	2329
cttattgaac aattttgctg actttcccta gtaatatctt aagtatatta actggaatca	2389
aatttgattt atagtttagaa gccaaactata ttgccagttt gtattgtttg aaataactgg	2449
aaaggcctga cctacatcgt ggggtaattt aacagaagct ctttccattt tttgttggtg	2509
ttgttaaaga gttttgttta tgaatgtggt ataaaaagaa aataaaaagt tataattttg	2569
acggaaaa	2577
<210> 4	
<211> 563	
<212> PRT	
<213> Rattus norvegicus	

<400> 4

Met Gly Asn Trp Leu Val Asn His Trp Leu Ser Val Leu Phe Leu Val
 1 5 10 15

Ser Trp Leu Gly Leu Asn Ile Phe Leu Phe Val Tyr Val Phe Leu Asn
 20 25 30

Tyr Glu Lys Ser Asp Lys Tyr Tyr Thr Arg Glu Ile Leu Gly Thr
 35 40 45

Ala Leu Ala Leu Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
 50 55 60

Met Val Ile Leu Ile Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
 65 70 75 80

Gly Thr Cys Ser Phe Cys Asn His Thr Leu Arg Lys Pro Leu Asp His
 85 90 95

Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Ile Phe Thr
 100 105 110

Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Glu Arg Tyr Ser Arg
 115 120 125

Ser Gln Gln Ala Met Asp Gly Ser Leu Ala Ser Val Leu Ser Ser Leu
 130 135 140

Phe His Pro Glu Lys Glu Asp Ser Trp Leu Asn Pro Ile Gln Ser Pro
 145 150 155 160

Asn Val Thr Val Met Tyr Ala Ala Phe Thr Ser Ile Ala Gly Leu Thr
 165 170 175

Gly Val Val Ala Thr Val Ala Leu Val Leu Met Val Thr Ser Ala Met
 180 185 190

Glu Phe Ile Arg Arg Asn Tyr Phe Glu Leu Phe Trp Tyr Thr His His
 195 200 205

Leu Phe Ile Ile Tyr Ile Ile Cys Leu Gly Ile His Gly Leu Gly Gly
 210 215 220

Ile Val Arg Gly Gln Thr Glu Glu Ser Met Ser Glu Ser His Pro Arg
 225 230 235 240

Asn Cys Ser Tyr Ser Phe His Glu Trp Asp Lys Tyr Glu Arg Ser Cys
 245 250 255

0701012W01.ST25.txt

Arg Ser Pro His Phe Val Gly Gln Pro Pro Glu Ser Trp Lys Trp Ile
260 265 270

Leu Ala Pro Ile Ala Phe Tyr Ile Phe Glu Arg Ile Leu Arg Phe Tyr
275 280 285

Arg Ser Arg Gln Lys Val Val Ile Thr Lys Val Val Met His Pro Cys
290 295 300

Lys Val Leu Glu Leu Gln Met Arg Lys Arg Gly Phe Thr Met Gly Ile
305 310 315 320

Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Phe Leu Glu Trp
325 330 335

His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Glu Phe Phe Ser Ile
340 345 350

His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Thr Phe
355 360 365

Glu Gln Gln His Ser Pro Met Pro Arg Ile Glu Val Asp Gly Pro Phe
370 375 380

Gly Thr Val Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu Val
385 390 395 400

Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Phe Leu Lys Ser Ile
405 410 415

Trp Tyr Lys Phe Gln Arg Ala His Asn Lys Leu Lys Thr Gln Lys Ile
420 425 430

Tyr Phe Tyr Trp Ile Cys Arg Glu Thr Gly Ala Phe Ala Trp Phe Asn
435 440 445

Asn Leu Leu Asn Ser Leu Glu Gln Glu Met Asp Glu Leu Gly Lys Pro
450 455 460

Asp Phe Leu Asn Tyr Arg Leu Phe Leu Thr Gly Trp Asp Ser Asn Ile
465 470 475 480

Ala Gly His Ala Ala Leu Asn Phe Asp Arg Ala Thr Asp Val Leu Thr
485 490 495

Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu
500 505 510

Phe Ser Arg Ile Ala Thr Ala His Pro Lys Ser Val Val Gly Val Phe

Leu Cys Gly Pro Pro Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys Arg
530 535 540

Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe Asn Lys
545 550 555 560

Glu Thr Phe

<210> 5

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for Nox1 gene

<400> 5

ggagcaggaa ttgggggtcac

20

<210> 6

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for Nox1 gene

<400> 6

ttgctgtccc atccggtgag

20

<210> 7

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for human Nox1 gene

<400> 7

ccactgtagg cgccctaagt t

21

<210> 8
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Reverse primer for human Nox1 gene
 <400> 8
 aagaatgacc ggtgcaagga 20

<210> 9
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> TaqMan probe
 <400> 9
 aagggcatcc ccctgagtct tggaa 25

<210> 10
 <211> 58
 <212> DNA
 <213> Artificial sequence

<220>
 <223> siRNA for human Nox1 gene
 <400> 10
 gcgtggcttc agcatggaat tcaagagatt ccatgctgaa gccacgcttt tttggaaa 58

<210> 11
 <211> 58
 <212> DNA
 <213> Artificial sequence

<220>

<223> siRNA for human Nox1 gene

<400> 11
gggctttcga acaacaatat tcaagagata ttgttggtcg aaagcccttt tttggaaa 58

<210> 12

<211> 59

<212> DNA

<213> Artificial sequence

<220>

<223> siRNA for rat Nox1 gene

<400> 12
gttatgagaa gtctgacaag ttcaagagac ttgtcagact ttcataatt ttttggaaa 59

<210> 13

<211> 58

<212> DNA

<213> Artificial sequence

<220>

<223> siRNA for rat Nox1 gene

<400> 13
gattcttggc taaatcccat tcaagagatg ggatttagcc aagaatcttt tttggaaa 58

<210> 14

<211> 58

<212> DNA

<213> Artificial sequence

<220>

<223> siRNA for rat Nox1 gene

<400> 14
ggacatttga acaacagcat tcaagagatg ctgttggtca aatgtccttt tttggaaa 58

<210> 15

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> Forward primer for Nox1 gene

<400> 15
ggcactccc ttgcttcca 20

<210> 16

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> Reverse primer for rat Nox1 gene

<400> 16
ggcaaaggca cctgtctctc t 21

<210> 17

<211> 20

<212> DNA

<213> Artificial sequence

<220>

<223> TaqManMGB probe

<400> 17
tccagtagaa atagatcttt 20

<210> 18

<211> 65

<212> DNA

<213> Artificial sequence

<220>

<223> siRNA construction

<400> 18
gatcccgtta tgagaagtct gacaagttca agagacttgt cagacttctc ataatttttt 60
ggaaa 65

<210> 19
 <211> 65
 <212> DNA
 <213> Artificial sequence

<220>

<223> siRNA construction

<400> 19
 agctttttcca aaaaattatg agaagtctga caagtctctt gaacttgtca gacttctcat 60
 aacgg 65

<210> 20
 <211> 64
 <212> DNA
 <213> Artificial sequence

<220>

<223> siRNA construction

<400> 20
 gatccccgatt cttggctaaa tccattcaa gagatgggat ttagccaaga atcttttttg 60
 gaaa 64

<210> 21
 <211> 64
 <212> DNA
 <213> Artificial sequence

<220>

<223> siRNA construction

<400> 21
 agctttttcca aaaaagattc ttggctaaat cccatctctt gaatgggatt tagccaagaa 60
 tcgg 64

<210> 22
 <211> 64
 <212> DNA

<213> Artificial sequence

<220>

<223> siRNA construction

<400> 22
gatcccgac atttgaacaa cagcattcaa gagatgctgt tgttcaaatg tccttttttg 60
gaaa 64

<210> 23

<211> 64

<212> DNA

<213> Artificial sequence

<220>

<223> siRNA construction

<400> 23
agctttttcca aaaaaggaca tttgaacaac agcatctctt gaatgctgtt gttcaaattgt 60
ccgg 64

<210> 24

<211> 17

<212> DNA

<213> Artificial sequence

<220>

<223> M13 primer

<400> 24
gttttccag tcacgac 17

<210> 25

<211> 21

<212> DNA

<213> Artificial sequence

<220>

<223> 3.0 Rev primer

<400> 25

	0701012w01.ST25.txt	
gagttagctc actcattagg c		21
<210> 26		
<211> 19		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Forward primer for Nox1 gene		
<400> 26		
atgggaaact ggctggta		19
<210> 27		
<211> 21		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Reverse primer for Nox1 gene		
<400> 27		
tcagaacggtt tctttgttga a		21